

SEQUENCE LISTING

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<120> Methods of Refolding Mammalian Glycosyltransferases

<130> 019957-016830US

<140> US 10/587,769
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<150> US 60/542,210
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<160> 80

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<210> 1
 <211> 445
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human beta-1,2-N-acetylglucosaminyltransferase I
 (GnTI, GnT1)

<400> 1
 Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
 1 5 10 15
 Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro
 20 25 30
 Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala
 35 40 45
 Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
 50 55 60
 Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser
 65 70 75 80
 Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg
 85 90 95

Val	Pro	Val	Thr	Pro	Ala	Pro	Ala	Val	Ile	Pro	Ile	Leu	Val	Ile	Ala	
			100					105					110			
Cys	Asp	Arg	Ser	Thr	Val	Arg	Arg	Cys	Leu	Asp	Lys	Leu	Leu	His	Tyr	
		115					120					125				
Arg	Pro	Ser	Ala	Glu	Leu	Phe	Pro	Ile	Ile	Val	Ser	Gln	Asp	Cys	Gly	
	130					135					140					
His	Glu	Glu	Thr	Ala	Gln	Ala	Ile	Ala	Ser	Tyr	Gly	Ser	Ala	Val	Thr	
145					150					155					160	
His	Ile	Arg	Gln	Pro	Asp	Leu	Ser	Ser	Ile	Ala	Val	Pro	Pro	Asp	His	
			165						170					175		
Arg	Lys	Phe	Gln	Gly	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Arg	Trp	Ala	
			180					185						190		
Leu	Gly	Gln	Val	Phe	Arg	Gln	Phe	Arg	Phe	Pro	Ala	Ala	Val	Val	Val	
		195					200					205				
Glu	Asp	Asp	Leu	Glu	Val	Ala	Pro	Asp	Phe	Phe	Glu	Tyr	Phe	Arg	Ala	
	210					215					220					
Thr	Tyr	Pro	Leu	Leu	Lys	Ala	Asp	Pro	Ser	Leu	Trp	Cys	Val	Ser	Ala	
225					230					235					240	
Trp	Asn	Asp	Asn	Gly	Lys	Glu	Gln	Met	Val	Asp	Ala	Ser	Arg	Pro	Glu	
				245					250					255		
Leu	Leu	Tyr	Arg	Thr	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Leu	Leu	Leu	
			260					265					270			
Ala	Glu	Leu	Trp	Ala	Glu	Leu	Glu	Pro	Lys	Trp	Pro	Lys	Ala	Phe	Trp	
		275					280					285				
Asp	Asp	Trp	Met	Arg	Arg	Pro	Glu	Gln	Arg	Gln	Gly	Arg	Ala	Cys	Ile	
	290					295					300					
Arg	Pro	Glu	Ile	Ser	Arg	Thr	Met	Thr	Phe	Gly	Arg	Lys	Gly	Val	Ser	
305					310					315					320	
His	Gly	Gln	Phe	Phe	Asp	Gln	His	Leu	Lys	Phe	Ile	Lys	Leu	Asn	Gln	
				325					330					335		
Gln	Phe	Val	His	Phe	Thr	Gln	Leu	Asp	Leu	Ser	Tyr	Leu	Gln	Arg	Glu	
			340					345					350			
Ala	Tyr	Asp	Arg	Asp	Phe	Leu	Ala	Arg	Val	Tyr	Gly	Ala	Pro	Gln	Leu	
		355					360					365				
Gln	Val	Glu	Lys	Val	Arg	Thr	Asn	Asp	Arg	Lys	Glu	Leu	Gly	Glu	Val	
	370					375					380					
Arg	Val	Gln	Tyr	Thr	Gly	Arg	Asp	Ser	Phe	Lys	Ala	Phe	Ala	Lys	Ala	
385					390					395					400	
Leu	Gly	Val	Met	Asp	Asp	Leu	Lys	Ser	Gly	Val	Pro	Arg	Ala	Gly	Tyr	
				405					410					415		

Arg Gly Ile Val Thr Phe Gln Phe Arg Gly Arg Arg Val His Leu Ala
420 425 430

Pro Pro Pro Thr Trp Glu Gly Tyr Asp Pro Ser Trp Asn
435 440 445

<210> 2

<211> 447

<212> PRT

<213> Oryctolagus cuniculus

<220>

<223> rabbit beta-1,2-N-acetylglucosaminyltransferase I
(GnTI, GnT1)

<400> 2

Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
1 5 10 15

Phe Val Ala Trp Asn Ala Leu Leu Leu Leu Phe Phe Trp Thr Arg Pro
20 25 30

Val Pro Ser Arg Leu Pro Ser Asp Asn Ala Leu Asp Asp Asp Pro Ala
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Arg Glu His His Ala
65 70 75 80

Leu Trp Ser Gln Arg Trp Lys Val Pro Thr Ala Ala Pro Pro Ala Gln
85 90 95

Pro His Val Pro Val Thr Pro Pro Pro Ala Val Ile Pro Ile Leu Val
100 105 110

Ile Ala Cys Asp Arg Ser Thr Val Arg Arg Cys Leu Asp Lys Leu Leu
115 120 125

His Tyr Arg Pro Ser Ala Glu Leu Phe Pro Ile Ile Val Ser Gln Asp
130 135 140

Cys Gly His Glu Glu Thr Ala Gln Val Ile Ala Ser Tyr Gly Ser Ala
145 150 155 160

Val Thr His Ile Arg Gln Pro Asp Leu Ser Asn Ile Ala Val Gln Pro
165 170 175

Asp His Arg Lys Phe Gln Gly Tyr Tyr Lys Ile Ala Arg His Tyr Arg
180 185 190

Trp Ala Leu Gly Gln Ile Phe His Asn Phe Asn Tyr Pro Ala Ala Val
195 200 205

Val Val Glu Asp Asp Leu Glu Val Ala Pro Asp Phe Phe Glu Tyr Phe
210 215 220

Gln Ala Thr Tyr Pro Leu Leu Lys Ala Asp Pro Ser Leu Trp Cys Val
225 230 235 240

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60
 Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80
 Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95
 Phe Arg Phe Pro Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110
 Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125
 Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140
 Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160
 Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175
 Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190
 Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205
 Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220
 His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240
 Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255
 Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270
 Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285
 Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300
 Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320
 Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335
 Tyr Asp Pro Ser Trp Asn
 340

<210> 4
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Ser mutant

<400> 4
 gcggtgattc ccacacctggt catcgccctgt gaccgcagca ctgttcggcg ctctctagac 60
 aagctgctgc attatcggcc ctcggtctgag ctcttcccca tcatcgttag ccaggactgc 120
 gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180
 cagccccgacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240
 aagatcgcgcg gccactaccg ctgggcgctg ggccaggctc tccggcagtt tcgcttcccc 300
 gcggccgctgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360
 gccacctatc cgctgctgaa ggccgacccc tccctgtggt gcgtctcggc ctggaatgac 420
 aacggcaagg agcagatggt ggacgccagc aggcctgagc tgctctaccg caccgacttt 480
 ttccctggcc tgggctggct gctggtggcc gagctctggg ctgagctgga gcccaagtgg 540
 ccaaaggcct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcgggcctgc 600
 atacgccctg agatctcaag aacgatgacc tttggccgca aggggtgtgag ccacgggcag 660
 ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcaccag 720
 ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780
 ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctgggggag 840
 gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
 atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
 ttcccgggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
 tgggaattag 1029

<210> 5
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unpaired
 cysteine mutation Cys121Ser mutant region

<400> 5
 Ser Thr Val Arg Arg Ser Leu Asp Lys Leu Leu His
 1 5 10

<210> 6
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Asp mutant

<400> 6
 Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
 1 5 10 15
 Arg Asp Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
 20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45
 Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60
 Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80
 Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95
 Phe Arg Phe Pro Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110
 Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125
 Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140
 Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160
 Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175
 Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190
 Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205
 Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220
 His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240
 Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255
 Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270
 Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285
 Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300
 Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320
 Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335
 Tyr Asp Pro Ser Trp Asn
 340

<210> 7
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Asp mutant

<400> 7
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 aagctgctgc attatcggcc ctcggtgag ctcttcccca tcatcgtag ccaggactgc 120
 gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180
 cagcccagacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240
 aagatcgcgc gccactaccg ctgggcgctg ggccaggtct tccggcagtt tcgcttcccc 300
 gcggccgtgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360
 gccacctatc cgctgctgaa ggccgacccc tccctgtggt gcgtctcggc ctggaatgac 420
 aacggcaagg agcagatggt ggacgocagc aggcctgagc tgctctaccg caccgacttt 480
 ttccctggcc tgggctggct gctgttggcc gagctctggg ctgagctgga gcccaagtgg 540
 ccaaaggcct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcgggcctgc 600
 atacgcctg agatctcaag aacgatgacc tttggccgca aggggtgtgag ccacgggcag 660
 ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcaccag 720
 ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780
 ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctgggggag 840
 gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
 atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
 ttcccgggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
 tgaattag 1029

<210> 8
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unpaired
 cysteine mutation Cys121Asp mutant region

<400> 8
 Ser Thr Val Arg Arg Asp Leu Asp Lys Leu Leu His
 1 5 10

<210> 9
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Thr mutant

<400> 9
 Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
 1 5 10 15
 Arg Thr Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
 20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45
 Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60
 Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80
 Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95
 Phe Arg Phe Pro Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110
 Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125
 Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140
 Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160
 Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175
 Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190
 Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205
 Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220
 His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240
 Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255
 Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270
 Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285
 Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300
 Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320
 Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335
 Tyr Asp Pro Ser Trp Asn
 340

<210> 10
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Thr mutant

<400> 10
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 aagctgctgc attatcggcc ctcggtgag ctcttcccca tcatacgtag ccaggactgc 120
 gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180
 cagcccgacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240
 aagatcgcgc gccactaccg ctgggcgctg ggccaggtct tccggcagtt tcgcttcccc 300
 gcggccgtgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360
 gccacctatc cgctgctgaa ggccgacccc tccctgtggt gcgtctcggc ctggaatgac 420
 aacggcaagg agcagatggt ggacgccagc aggcctgagc tgctctaccg caccgacttt 480
 ttccctggcc tgggctggct gctgttggcc gagctctggg ctgagctgga gcccaagtgg 540
 ccaaaggcct tctgggacga ctggatgcgg cgcccgagc agcggcaggg gcgggcctgc 600
 atacgcctct agatctcaag aacgatgacc tttggccgca aggggtgtgag ccacgggcag 660
 ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcaccag 720
 ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780
 ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctgggggag 840
 gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
 atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
 ttcccgggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
 tggaattag 1029

<210> 11
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unpaired
 cysteine mutation Cys121Thr mutant region

<400> 11
 Ser Thr Val Arg Arg Thr Leu Asp Lys Leu Leu His
 1 5 10

<210> 12
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Ala mutant

<400> 12
 Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
 1 5 10 15
 Arg Ala Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
 20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45
 Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60
 Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80
 Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95
 Phe Arg Phe Pro Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110
 Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125
 Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140
 Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160
 Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175
 Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190
 Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205
 Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220
 His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240
 Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255
 Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270
 Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285
 Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300
 Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320
 Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335
 Tyr Asp Pro Ser Trp Asn
 340

<210> 13
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Ala mutant

<400> 13
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 aagctgctgc attatcggcc ctcggtgag ctcttcccca tcatcgttag ccaggactgc 120
 gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180
 cagcccgacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240
 aagatcgcgc gccactaccg ctgggcgctg ggccaggtct tccggcagtt tcgcttcccc 300
 gcggccgtgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360
 gccacctatc cgctgctgaa ggccgacccc tccctgtggt gcgtctcggc ctggaatgac 420
 aacggcaagg agcagatggt ggacgccagc aggcctgagc tgctctaccg caccgacttt 480
 ttccctggcc tgggctggct gctgttggcc gagctctggg ctgagctgga gcccaagtgg 540
 ccaaaggcct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcgggcctgc 600
 atacgccttg agatctcaag aacgatgacc tttggccgca aggggtgtgag ccacgggcag 660
 ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcaccacg 720
 ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780
 ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctggggggag 840
 gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
 atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
 ttcccgggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
 tgggaattag 1029

<210> 14
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unpaired
 cysteine mutation Cys121Ala mutant region

<400> 14
 Ser Thr Val Arg Arg Ala Leu Asp Lys Leu Leu His
 1 5 10

<210> 15
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Arg120Ala Cys121His double mutant

<400> 15
 Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
 1 5 10 15
 Ala His Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
 20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45
 Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60
 Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80
 Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95
 Phe Arg Phe Pro Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110
 Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125
 Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140
 Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160
 Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175
 Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190
 Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205
 Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220
 His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240
 Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255
 Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270
 Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285
 Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300
 Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320
 Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335
 Tyr Asp Pro Ser Trp Asn
 340

<210> 16
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Arg120Ala Cys121His double mutant

<400> 16
 gcggtgattc ccatacctggt catcgccctgt gaccgcagca ctgttcgggc ccacctagac 60
 aagctgctgc attatcggcc ctcggtgag ctcttcccca tcatcgttag ccaggactgc 120
 gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180
 cagcccgacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240
 aagatcgcgc gccactaccg ctgggcgctg ggccaggctt tccggcagtt tcgcttcccc 300
 gcggccgtgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360
 gccacctatc cgctgctgaa ggccgacccc tccctgtggt gcgtctcggc ctggaatgac 420
 aacggcaagg agcagatggt ggacgccagc aggcctgagc tgctctaccg caccgacttt 480
 ttccctggcc tgggctggct gctgttggcc gagctctggg ctgagctgga gcccaagtgg 540
 ccaaaggcct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcgggcctgc 600
 atacgccttg agatctcaag aacgatgacc tttggccgca aggggtgtgag ccacgggcag 660
 ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcaccag 720
 ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780
 ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctggggggag 840
 gtgcgggtgc agtatacggg caggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
 atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
 ttcccgggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
 tgaattag 1029

<210> 17
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unpaired
 cysteine mutation Arg120Ala Cys121His double
 mutant region

<400> 17
 Ser Thr Val Arg Ala His Leu Asp Lys Leu Leu His
 1 5 10

<210> 18
 <211> 374
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat liver Gal beta-1,3-GalNAc
 alpha-2,3-sialyltransferase III (ST3GalIII)

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> delta28 deletion

<400> 18

Met Gly Leu Leu Val Phe Val Arg Asn Leu Leu Leu Ala Leu Cys Leu
1 5 10 15

Phe Leu Val Leu Gly Phe Leu Tyr Tyr Ser Ala Trp Lys Leu His Leu
20 25 30

Leu Gln Trp Glu Asp Ser Asn Ser Leu Ile Leu Ser Leu Asp Ser Ala
35 40 45

Gly Gln Thr Leu Gly Thr Glu Tyr Asp Arg Leu Gly Phe Leu Leu Lys
50 55 60

Leu Asp Ser Lys Leu Pro Ala Glu Leu Ala Thr Lys Tyr Ala Asn Phe
65 70 75 80

Ser Glu Gly Ala Cys Lys Pro Gly Tyr Ala Ser Ala Met Met Thr Ala
85 90 95

Ile Phe Pro Arg Phe Ser Lys Pro Ala Pro Met Phe Leu Asp Asp Ser
100 105 110

Phe Arg Lys Trp Ala Arg Ile Arg Glu Phe Val Pro Pro Phe Gly Ile
115 120 125

Lys Gly Gln Asp Asn Leu Ile Lys Ala Ile Leu Ser Val Thr Lys Glu
130 135 140

Tyr Arg Leu Thr Pro Ala Leu Asp Ser Leu His Cys Arg Arg Cys Ile
145 150 155 160

Ile Val Gly Asn Gly Gly Val Leu Ala Asn Lys Ser Leu Gly Ser Arg
165 170 175

Ile Asp Asp Tyr Asp Ile Val Ile Arg Leu Asn Ser Ala Pro Val Lys
180 185 190

Gly Phe Glu Lys Asp Val Gly Ser Lys Thr Thr Leu Arg Ile Thr Tyr
195 200 205

Pro Glu Gly Ala Met Gln Arg Pro Glu Gln Tyr Glu Arg Asp Ser Leu
210 215 220

Phe Val Leu Ala Gly Phe Lys Trp Gln Asp Phe Lys Trp Leu Lys Tyr
225 230 235 240

Ile Val Tyr Lys Glu Arg Val Ser Ala Ser Asp Gly Phe Trp Lys Ser
245 250 255

Val Ala Thr Arg Val Pro Lys Glu Pro Pro Glu Ile Arg Ile Leu Asn
260 265 270

Pro Tyr Phe Ile Gln Glu Ala Ala Phe Thr Leu Ile Gly Leu Pro Phe
275 280 285

Asn Asn Gly Leu Met Gly Arg Gly Asn Ile Pro Thr Leu Gly Ser Val
290 295 300

Ala Val Thr Met Ala Leu Asp Gly Cys Asp Glu Val Ala Val Ala Gly
305 310 315 320

Val	Arg	Gly	Ala	Asp	Ala	Ala	Gln	Ala	Lys	Val	Leu	Thr	Phe	Leu	Asp
210						215					220				
Ser	His	Cys	Glu	Cys	Asn	Glu	His	Trp	Leu	Glu	Pro	Leu	Leu	Glu	Arg
225					230					235					240
Val	Ala	Glu	Asp	Arg	Thr	Arg	Val	Val	Ser	Pro	Ile	Ile	Asp	Val	Ile
				245					250					255	
Asn	Met	Asp	Asn	Phe	Gln	Tyr	Val	Gly	Ala	Ser	Ala	Asp	Leu	Lys	Gly
			260					265					270		
Gly	Phe	Asp	Trp	Asn	Leu	Val	Phe	Lys	Trp	Asp	Tyr	Met	Thr	Pro	Glu
		275					280					285			
Gln	Arg	Arg	Ser	Arg	Gln	Gly	Asn	Pro	Val	Ala	Pro	Ile	Lys	Thr	Pro
	290					295					300				
Met	Ile	Ala	Gly	Gly	Leu	Phe	Val	Met	Asp	Lys	Phe	Tyr	Phe	Glu	Glu
305					310					315					320
Leu	Gly	Lys	Tyr	Asp	Met	Met	Met	Asp	Val	Trp	Gly	Gly	Glu	Asn	Leu
				325					330					335	
Glu	Ile	Ser	Phe	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Leu	Glu	Ile	Ile
			340					345					350		
Pro	Cys	Ser	Arg	Val	Gly	His	Val	Phe	Arg	Lys	Gln	His	Pro	Tyr	Thr
		355					360					365			
Phe	Pro	Gly	Gly	Ser	Gly	Thr	Val	Phe	Ala	Arg	Asn	Thr	Arg	Arg	Ala
	370					375					380				
Ala	Glu	Val	Trp	Met	Asp	Glu	Tyr	Lys	Asn	Phe	Tyr	Tyr	Ala	Ala	Val
385					390					395					400
Pro	Ser	Ala	Arg	Asn	Val	Pro	Tyr	Gly	Asn	Ile	Gln	Ser	Arg	Leu	Glu
				405					410					415	
Leu	Arg	Lys	Lys	Leu	Ser	Cys	Lys	Pro	Phe	Lys	Trp	Tyr	Leu	Glu	Asn
			420					425					430		
Val	Tyr	Pro	Glu	Leu	Arg	Val	Pro	Asp	His	Gln	Asp	Ile	Ala	Phe	Gly
		435					440					445			
Ala	Leu	Gln	Gln	Gly	Thr	Asn	Cys	Leu	Asp	Thr	Leu	Gly	His	Phe	Ala
	450					455					460				
Asp	Gly	Val	Val	Gly	Val	Tyr	Glu	Cys	His	Asn	Ala	Gly	Gly	Asn	Gln
465					470					475					480
Glu	Trp	Ala	Leu	Thr	Lys	Glu	Lys	Ser	Val	Lys	His	Met	Asp	Leu	Cys
				485					490					495	
Cys	Arg	Glu	Asn	Asp	Ser	Arg	Gln	Lys	Trp	Glu	Gln	Ile	Glu	Gly	Asn
			500					505					510		
Ser	Lys	Leu	Arg	His	Val	Gly	Ser	Asn	Leu	Cys	Leu	Asp	Ser	Arg	Thr
		515					520					525			

Ala Lys Ser Gly Gly Leu Ser Val Glu Val Cys Gly Pro Ala Leu Ser
 530 535 540

Gln Gln Trp Lys Phe Thr Leu Asn Leu Gln Gln
 545 550 555

<210> 20
 <211> 1713
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human full-length
 UDP-N-acetylgalactosaminyltransferase 2 (GalNAcT2)

<400> 20
 atgcggcgcc gctcgcggat gctgctctgc ttcgccttcc tgtgggtgct gggcatcgcc 60
 tactacatgt actcgggggg cggctctgcg ctggccgggg gcgcggggcg cggcgccggc 120
 aggaaggagg actggaatga aattgacccc attaaaaaga aagaccttca tcacagcaat 180
 ggagaagaga aagcacaaag catggagacc ctccctccag ggaaagtacg gtggccagac 240
 ttttaaccagg aagcttatgt tggagggacg atggtccgct ccgggcagga cccttacgcc 300
 cgcaacaagt tcaaccaggt ggagagtgat aagcttcgaa tggacagagc catccctgac 360
 acccggcgatg accagtgtca gcggaagcag tggcggggtg atctgccggc caccagcgtg 420
 gtgatcacgt ttcacaatga agccagggtcg gccctactca ggaccgtggt cagcgtgctt 480
 aagaaaagcc cgccccatct cataaaagaa atcatcttgg tggatgacta cagcaatgat 540
 cctgaggacg gggctctctt ggggaaaatt gagaaagtgc gagttcttag aaatgatcga 600
 cgagaaggcc tcatgcgctc acgggttcgg ggggccgatg ctgccaagc caaggctctg 660
 accttcctgg acagtcactg cgagtgtaat gagcactggc tggagccccct cctggaaagg 720
 gtggcgaggg acaggactcg ggttgtgtca cccatcatcg atgtcattaa tatggacaac 780
 tttcagtatg tgggggcacg tgctgacttg aagggcgggt ttgattggaa cttggtattc 840
 aagtgggatt acatgacgcc tgagcagaga aggtcccggc aggggaacct agtcgccct 900
 ataaaaacct ccatgattgc tgggtgggctg tttgtgatgg ataagttcta ttttgaagaa 960
 ctggggaagt acgacatgat gatggatgtg tggggaggag agaacctaga gatctcgttc 1020
 cgcgtgtggc agtgtggtg cagcctggag atcatcccgt gcagccgtgt gggacacgtg 1080
 ttccggaagc agcaccctca cacgttcccg ggtggcagt gcactgtctt tgcccgaac 1140
 acccgccggg cagcagaggt ctggatggat gaatacaaaa atttctatta tgcagcagt 1200
 ccttctgcta gaaacgttcc ttatggaaat attcagagca gattggagct taggaagaaa 1260
 ctgagctgca agcctttcaa atggtacctt gaaaatgtct atccagagtt aagggttcca 1320
 gaccatcagg atatagcttt tggggccttg cagcagggaa ctaactgcct cgacactttg 1380
 ggacactttg ctgatggtg ggttggagtt tatgaatgtc acaatgctgg gggaaaccag 1440
 gaatgggcct tgacgaagga gaagtcggtg aagcacatgg atttgtgcct tactgtggtg 1500
 gaccgggcac cgggctctct tataaagctg cagggtctgc gagaaaatga cagcagacag 1560
 aaatgggaac agatcgaggg caactccaag ctgaggcacg tgggcagcaa cctgtgcctg 1620
 gacagtcgca cggccaagag cgggggccta agcgtggagg tgtgtggccc ggccctttcg 1680
 cagcagtgga agttcacgct caacctgcag cag 1713

<210> 21
 <211> 520
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:delta51
 UDP-N-acetylgalactosaminyltransferase 2
 (delta51GalNAcT2)

<400> 21
 Lys Lys Lys Asp Leu His His Ser Asn Gly Glu Glu Lys Ala Gln Ser
 1 5 10 15

Met Glu Thr Leu Pro Pro Gly Lys Val Arg Trp Pro Asp Phe Asn Gln
 20 25 30
 Glu Ala Tyr Val Gly Gly Thr Met Val Arg Ser Gly Gln Asp Pro Tyr
 35 40 45
 Ala Arg Asn Lys Phe Asn Gln Val Glu Ser Asp Lys Leu Arg Met Asp
 50 55 60
 Arg Ala Ile Pro Asp Thr Arg His Asp Gln Cys Gln Arg Lys Gln Trp
 65 70 75 80
 Arg Val Asp Leu Pro Ala Thr Ser Val Val Ile Thr Phe His Asn Glu
 85 90 95
 Ala Arg Ser Ala Leu Leu Arg Thr Val Val Ser Val Leu Lys Lys Ser
 100 105 110
 Pro Pro His Leu Ile Lys Glu Ile Ile Leu Val Asp Asp Tyr Ser Asn
 115 120 125
 Asp Pro Glu Asp Gly Ala Leu Leu Gly Lys Ile Glu Lys Val Arg Val
 130 135 140
 Leu Arg Asn Asp Arg Arg Glu Gly Leu Met Arg Ser Arg Val Arg Gly
 145 150 155 160
 Ala Asp Ala Ala Gln Ala Lys Val Leu Thr Phe Leu Asp Ser His Cys
 165 170 175
 Glu Cys Asn Glu His Trp Leu Glu Pro Leu Leu Glu Arg Val Ala Glu
 180 185 190
 Asp Arg Thr Arg Val Val Ser Pro Ile Ile Asp Val Ile Asn Met Asp
 195 200 205
 Asn Phe Gln Tyr Val Gly Ala Ser Ala Asp Leu Lys Gly Gly Phe Asp
 210 215 220
 Trp Asn Leu Val Phe Lys Trp Asp Tyr Met Thr Pro Glu Gln Arg Arg
 225 230 235 240
 Ser Arg Gln Gly Asn Pro Val Ala Pro Ile Lys Thr Pro Met Ile Ala
 245 250 255
 Gly Gly Leu Phe Val Met Asp Lys Phe Tyr Phe Glu Glu Leu Gly Lys
 260 265 270
 Tyr Asp Met Met Met Asp Val Trp Gly Gly Glu Asn Leu Glu Ile Ser
 275 280 285
 Phe Arg Val Trp Gln Cys Gly Gly Ser Leu Glu Ile Ile Pro Cys Ser
 290 295 300
 Arg Val Gly His Val Phe Arg Lys Gln His Pro Tyr Thr Phe Pro Gly
 305 310 315 320
 Gly Ser Gly Thr Val Phe Ala Arg Asn Thr Arg Arg Ala Ala Glu Val
 325 330 335

Trp Met Asp Glu Tyr Lys Asn Phe Tyr Tyr Ala Ala Val Pro Ser Ala
 340 345 350
 Arg Asn Val Pro Tyr Gly Asn Ile Gln Ser Arg Leu Glu Leu Arg Lys
 355 360 365
 Lys Leu Ser Cys Lys Pro Phe Lys Trp Tyr Leu Glu Asn Val Tyr Pro
 370 375 380
 Glu Leu Arg Val Pro Asp His Gln Asp Ile Ala Phe Gly Ala Leu Gln
 385 390 395 400
 Gln Gly Thr Asn Cys Leu Asp Thr Leu Gly His Phe Ala Asp Gly Val
 405 410 415
 Val Gly Val Tyr Glu Cys His Asn Ala Gly Gly Asn Gln Glu Trp Ala
 420 425 430
 Leu Thr Lys Glu Lys Ser Val Lys His Met Asp Leu Cys Leu Thr Val
 435 440 445
 Val Asp Arg Ala Pro Gly Ser Leu Ile Lys Leu Gln Gly Cys Arg Glu
 450 455 460
 Asn Asp Ser Arg Gln Lys Trp Glu Gln Ile Glu Gly Asn Ser Lys Leu
 465 470 475 480
 Arg His Val Gly Ser Asn Leu Cys Leu Asp Ser Arg Thr Ala Lys Ser
 485 490 495
 Gly Gly Leu Ser Val Glu Val Cys Gly Pro Ala Leu Ser Gln Gln Trp
 500 505 510
 Lys Phe Thr Leu Asn Leu Gln Gln
 515 520

<210> 22
 <211> 1560
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:delta51
 UDP-N-acetylgalactosaminyltransferase 2
 (delta51GalNAcT2)

<400> 22
 aaaaagaaag accttcacatca cagcaatgga gaagagaaag cacaaagcat ggagaccctc 60
 cctccaggga aagtacggtg gccagacttt aaccaggaag cttatgttgg agggacgatg 120
 gtccgctccg ggcaggaccc ttacgcccgc aacaagttca accaggtgga gagtgataag 180
 cttcgaatgg acagagccat ccctgacacc cggcatgacc agtgtcagcg gaagcagtgg 240
 cgggtggatc tgccggccac cagcgtggtg atcacgtttc acaatgaagc caggtcggcc 300
 ctactcagga ccgtggtcag cgtgcttaag aaaagcccgc cccatctcat aaaagaaatc 360
 atcttggtgg atgactacag caatgatcct gaggacgggg ctctcttggg gaaaattgag 420
 aaagtgcgag ttcttagaaa tgatcgacga gaaggcctca tgcgctcacg ggttcggggg 480
 gccgatgctg cccaagccaa ggtcctgacc ttcttgga gtcactgcga gtgtaattgag 540
 cactggctgg agcccctcct ggaaagggtg gcggaggaca ggactcgggt tgtgtcaccc 600
 atcatcgatg tcattaatat ggacaacttt cagtatgtgg gggcatctgc tgacttgaag 660
 ggcggttttg attggaactt ggtattcaag tgggattaca tgacgcctga gcagagaagg 720
 tcccggcagg ggaacccagt cgcccctata aaaaccccca tgattgctgg tgggctgttt 780

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gtgatggata agttctatatt tgaagaactg gggaagtacg acatgatgat ggatgtgtgg 840
ggaggagaga acctagagat ctggttccgc gtgtggcagt gtggtggcag cctggagatc 900
atcccgtgca gccgtgtggg acacgtgttc cggaagcagc acccctacac gttcccgggt 960
ggcagtggca ctgtctttgc ccgaaacacc cgccgggcag cagaggtctg gatggatgaa 1020
tacaaaaatt tctattatgc agcagtgcct tctgctagaa acgttcctta tggaaatatt 1080
cagagcagat tggagcttag gaagaaactc agctgcaagc ctttcaaagc gtaccttgaa 1140
aatgtctatc cagagttaag ggttccagac catcaggata tagcttttgg ggccttgca 1200
cagggaaacta actgcctcga cactttggga cactttgctg atggtgtggt tggagtatat 1260
gaatgtcaca atgctggggg aaaccaggaa tgggccttga cgaaggagaa gtcggtgaag 1320
cacatggatt tgtgccttac tgtggtggac cgggcaccgg gctctcttat aaagctgcag 1380
ggctgccgag aaaatgacag cagacagaaa tgggaacaga tgcagggcaa ctccaagctg 1440
aggcacgtgg gcagcaacct gtgcctggac agtcgcacgg ccaagagcgg gggcctaagc 1500
gtggagggtgt gtggcccggc cttttcgcag cagtggaaat tcacgctcaa cctgcagcag 1560

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<210> 23
 <211> 691
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:maltose binding
 protein-Gal beta-1,3-GalNAc
 alpha-2,3-sialyltransferase 1 (MBP-ST3Gal1) fusion
 protein

<400> 23
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175

Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	180	185	190
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	195	200	205
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	210	215	220
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	225	230	235
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	245	250	255
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	260	265	270
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	275	280	285
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	290	295	300
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	305	310	315
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln	325	330	335
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala	340	345	350
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn	355	360	365
Ser	Ser	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Leu	Gly	Ile	370	375	380
Glu	Gly	Arg	Ile	Ser	Glu	Phe	Gly	Ser	Glu	Leu	Ser	Glu	Asn	Phe	Lys	385	390	395
Lys	Leu	Met	Lys	Tyr	Pro	Tyr	Arg	Pro	Cys	Thr	Cys	Thr	Arg	Cys	Ile	405	410	415
Glu	Glu	Gln	Arg	Val	Ser	Ala	Trp	Phe	Asp	Glu	Arg	Phe	Asn	Arg	Ser	420	425	430
Met	Gln	Pro	Leu	Leu	Thr	Ala	Lys	Asn	Ala	His	Leu	Glu	Glu	Asp	Thr	435	440	445
Tyr	Lys	Trp	Trp	Leu	Arg	Leu	Gln	Arg	Glu	Lys	Gln	Pro	Asn	Asn	Leu	450	455	460
Asn	Asp	Thr	Ile	Arg	Glu	Leu	Phe	Gln	Val	Val	Pro	Gly	Asn	Val	Asp	465	470	475
Pro	Leu	Leu	Glu	Lys	Arg	Leu	Val	Ser	Cys	Arg	Arg	Cys	Ala	Val	Val	485	490	495

Gly Asn Ser Gly Asn Leu Lys Glu Ser Tyr Tyr Gly Pro Gln Ile Asp
 500 505 510
 Ser His Asp Phe Val Leu Arg Met Asn Lys Ala Pro Thr Glu Gly Phe
 515 520 525
 Glu Ala Asp Val Gly Ser Lys Thr Thr His His Phe Val Tyr Pro Glu
 530 535 540
 Ser Phe Arg Glu Leu Ala Gln Glu Val Ser Met Ile Leu Val Pro Phe
 545 550 555 560
 Lys Thr Thr Asp Leu Glu Trp Val Ile Ser Ala Thr Thr Thr Gly Arg
 565 570 575
 Ile Ser His Thr Tyr Val Pro Val Pro Ala Lys Ile Lys Val Lys Lys
 580 585 590
 Glu Lys Ile Leu Ile Tyr His Pro Ala Phe Ile Lys Tyr Val Phe Asp
 595 600 605
 Arg Trp Leu Gln Gly His Gly Arg Tyr Pro Ser Thr Gly Ile Leu Ser
 610 615 620
 Val Ile Phe Ser Leu His Ile Cys Asp Glu Val Asp Leu Tyr Gly Phe
 625 630 635 640
 Gly Ala Asp Ser Lys Gly Asn Trp His His Tyr Trp Glu Asn Asn Pro
 645 650 655
 Ser Ala Gly Ala Phe Arg Lys Thr Gly Val His Asp Gly Asp Phe Glu
 660 665 670
 Ser Asn Val Thr Thr Ile Leu Ala Ser Ile Asn Lys Ile Arg Ile Phe
 675 680 685
 Lys Gly Arg
 690

<210> 24
 <211> 841
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:maltose binding
 protein-starch binding domain-Gal beta-1,3-GalNAc
 alpha-2,3-sialyltransferase 1 (MBP-SBD-ST3Gal1)
 fusion protein

<400> 24
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365

Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
 370 375 380
 Glu Gly Arg Ile Ser Glu Phe Gly Ser Ile Val Ala Thr Gly Gly Thr
 385 390 395 400
 Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser Thr Ser
 405 410 415
 Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser Ser Thr
 420 425 430
 Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala
 435 440 445
 Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln
 450 455 460
 Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys
 465 470 475 480
 Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala
 485 490 495
 Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser
 500 505 510
 Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala
 515 520 525
 Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg Gly Ser Glu
 530 535 540
 Leu Ser Glu Asn Phe Lys Lys Leu Met Lys Tyr Pro Tyr Arg Pro Cys
 545 550 555 560
 Thr Cys Thr Arg Cys Ile Glu Glu Gln Arg Val Ser Ala Trp Phe Asp
 565 570 575
 Glu Arg Phe Asn Arg Ser Met Gln Pro Leu Leu Thr Ala Lys Asn Ala
 580 585 590
 His Leu Glu Glu Asp Thr Tyr Lys Trp Trp Leu Arg Leu Gln Arg Glu
 595 600 605
 Lys Gln Pro Asn Asn Leu Asn Asp Thr Ile Arg Glu Leu Phe Gln Val
 610 615 620
 Val Pro Gly Asn Val Asp Pro Leu Leu Glu Lys Arg Leu Val Ser Cys
 625 630 635 640
 Arg Arg Cys Ala Val Val Gly Asn Ser Gly Asn Leu Lys Glu Ser Tyr
 645 650 655
 Tyr Gly Pro Gln Ile Asp Ser His Asp Phe Val Leu Arg Met Asn Lys
 660 665 670
 Ala Pro Thr Glu Gly Phe Glu Ala Asp Val Gly Ser Lys Thr Thr His
 675 680 685

His Phe Val Tyr Pro Glu Ser Phe Arg Glu Leu Ala Gln Glu Val Ser
 690 695 700
 Met Ile Leu Val Pro Phe Lys Thr Thr Asp Leu Glu Trp Val Ile Ser
 705 710 715 720
 Ala Thr Thr Thr Gly Arg Ile Ser His Thr Tyr Val Pro Val Pro Ala
 725 730 735
 Lys Ile Lys Val Lys Lys Glu Lys Ile Leu Ile Tyr His Pro Ala Phe
 740 745 750
 Ile Lys Tyr Val Phe Asp Arg Trp Leu Gln Gly His Gly Arg Tyr Pro
 755 760 765
 Ser Thr Gly Ile Leu Ser Val Ile Phe Ser Leu His Ile Cys Asp Glu
 770 775 780
 Val Asp Leu Tyr Gly Phe Gly Ala Asp Ser Lys Gly Asn Trp His His
 785 790 795 800
 Tyr Trp Glu Asn Asn Pro Ser Ala Gly Ala Phe Arg Lys Thr Gly Val
 805 810 815
 His Asp Gly Asp Phe Glu Ser Asn Val Thr Thr Ile Leu Ala Ser Ile
 820 825 830
 Asn Lys Ile Arg Ile Phe Lys Gly Arg
 835 840

<210> 25
 <211> 793
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:maltose binding
 protein-alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I mouse truncation
 fusion protein (MBP-mST6GalNAcI S127)

<220>
 <221> MOD_RES
 <222> (708)
 <223> Xaa = any amino acid

<400> 25
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60

His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	65	70	75	80
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	85	90	95	
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	100	105	110	
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	115	120	125	
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	130	135	140	
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	145	150	155	160
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	165	170	175	
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	180	185	190	
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	195	200	205	
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	210	215	220	
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	225	230	235	240
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	245	250	255	
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	260	265	270	
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	275	280	285	
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	290	295	300	
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	305	310	315	320
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln	325	330	335	
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala	340	345	350	
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn	355	360	365	
Ser	Ser	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Leu	Gly	Ile	370	375	380	

Glu	Gly	Arg	Ile	Ser	Glu	Phe	Gly	Ser	Ser	Glu	His	Leu	Asp	Lys	Val	385	390	395	400
Pro	Arg	Thr	Pro	Gly	Ala	Leu	Ser	Thr	Arg	Lys	Thr	Pro	Met	Ala	Thr	405	410	415	
Gly	Ala	Val	Pro	Ala	Lys	Lys	Lys	Val	Val	Gln	Ala	Thr	Lys	Ser	Pro	420	425	430	
Ala	Ser	Ser	Pro	His	Pro	Thr	Thr	Arg	Arg	Arg	Gln	Arg	Leu	Lys	Ala	435	440	445	
Ser	Glu	Phe	Lys	Ser	Glu	Pro	Arg	Trp	Asp	Phe	Glu	Glu	Glu	Tyr	Ser	450	455	460	
Leu	Asp	Met	Ser	Ser	Leu	Gln	Thr	Asn	Cys	Ser	Ala	Ser	Val	Lys	Ile	465	470	475	480
Lys	Ala	Ser	Lys	Ser	Pro	Trp	Leu	Gln	Asn	Ile	Phe	Leu	Pro	Asn	Ile	485	490	495	
Thr	Leu	Phe	Leu	Asp	Ser	Gly	Arg	Phe	Thr	Gln	Ser	Glu	Trp	Asn	Arg	500	505	510	
Leu	Glu	His	Phe	Ala	Pro	Pro	Phe	Gly	Phe	Met	Glu	Leu	Asn	Gln	Ser	515	520	525	
Leu	Val	Gln	Lys	Val	Val	Thr	Arg	Phe	Pro	Pro	Val	Arg	Gln	Gln	Gln	530	535	540	
Leu	Leu	Leu	Ala	Ser	Leu	Pro	Thr	Gly	Tyr	Ser	Lys	Cys	Ile	Thr	Cys	545	550	555	560
Ala	Val	Val	Gly	Asn	Gly	Gly	Ile	Leu	Asn	Asp	Ser	Arg	Val	Gly	Arg	565	570	575	
Glu	Ile	Asp	Ser	His	Asp	Tyr	Val	Phe	Arg	Leu	Ser	Gly	Ala	Val	Ile	580	585	590	
Lys	Gly	Tyr	Glu	Gln	Asp	Val	Gly	Thr	Arg	Thr	Ser	Phe	Tyr	Gly	Phe	595	600	605	
Thr	Ala	Phe	Ser	Leu	Thr	Gln	Ser	Ile	Leu	Ile	Leu	Gly	Arg	Arg	Gly	610	615	620	
Phe	Gln	His	Val	Pro	Leu	Gly	Lys	Asp	Val	Arg	Tyr	Leu	His	Phe	Leu	625	630	635	640
Glu	Gly	Thr	Arg	Asn	Tyr	Glu	Trp	Leu	Glu	Ala	Met	Phe	Leu	Asn	Gln	645	650	655	
Thr	Leu	Ala	Lys	Thr	His	Leu	Ser	Trp	Phe	Arg	His	Arg	Pro	Gln	Glu	660	665	670	
Ala	Phe	Arg	Asn	Ala	Leu	Asp	Leu	Asp	Arg	Tyr	Leu	Leu	Leu	His	Pro	675	680	685	
Asp	Phe	Leu	Arg	Tyr	Met	Lys	Asn	Arg	Phe	Leu	Arg	Ser	Lys	Thr	Leu	690	695	700	

Asp Thr Ala Xaa Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu
 705 710 715 720
 Leu Leu Thr Ala Leu His Leu Cys Asp Lys Val Ser Ala Tyr Gly Phe
 725 730 735
 Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp Thr Ser
 740 745 750
 Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Arg Leu Glu Arg
 755 760 765
 Met Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile Trp Leu Tyr Gln
 770 775 780
 Arg Pro Gln Ser Asp Lys Ala Lys Asn
 785 790

<210> 26
 <211> 958
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:maltose binding
 protein-alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I human truncation
 fusion protein (MBP-hST6GalNAcI K36)

<400> 26
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
 370 375 380
 Glu Gly Arg Ile Ser Glu Phe Gly Ser Lys Glu Pro Gln Thr Lys Pro
 385 390 395 400
 Ser Arg His Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser
 405 410 415
 Leu Ala Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr
 420 425 430
 Ile Tyr Ala Glu Pro Val Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr
 435 440 445
 Gln Pro Lys Ala His Thr Thr Gly Asp Arg Gly Lys Glu Ala Asn Gln
 450 455 460
 Ala Pro Pro Glu Glu Gln Asp Lys Val Pro His Thr Ala Gln Arg Ala
 465 470 475 480

Ala Trp Lys Ser Pro Glu Lys Glu Lys Thr Met Val Asn Thr Leu Ser
 485 490 495
 Pro Arg Gly Gln Asp Ala Gly Met Ala Ser Gly Arg Thr Glu Ala Gln
 500 505 510
 Ser Trp Lys Ser Gln Asp Thr Lys Thr Thr Gln Gly Asn Gly Gly Gln
 515 520 525
 Thr Arg Lys Leu Thr Ala Ser Arg Thr Val Ser Glu Lys His Gln Gly
 530 535 540
 Lys Ala Ala Thr Thr Ala Lys Thr Leu Ile Pro Lys Ser Gln His Arg
 545 550 555 560
 Met Leu Ala Pro Thr Gly Ala Val Ser Thr Arg Thr Arg Gln Lys Gly
 565 570 575
 Val Thr Thr Ala Val Ile Pro Pro Lys Glu Lys Lys Pro Gln Ala Thr
 580 585 590
 Pro Pro Pro Ala Pro Phe Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg
 595 600 605
 Leu Lys Ala Ala Asn Phe Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu
 610 615 620
 Lys Tyr Ser Phe Glu Ile Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser
 625 630 635 640
 Val Lys Ile Lys Ala Ser Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu
 645 650 655
 Pro Asn Leu Thr Leu Phe Leu Asp Ser Arg His Phe Asn Gln Ser Glu
 660 665 670
 Trp Asp Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe Met Glu Leu
 675 680 685
 Asn Tyr Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro Val Pro
 690 695 700
 Gln Gln Gln Leu Leu Leu Ala Ser Leu Pro Ala Gly Ser Leu Arg Cys
 705 710 715 720
 Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn Asn Ser His
 725 730 735
 Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe Arg Leu Ser Gly
 740 745 750
 Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly Thr Arg Thr Ser Phe
 755 760 765
 Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln Ser Leu Leu Ile Leu Gly
 770 775 780
 Asn Arg Gly Phe Lys Asn Val Pro Leu Gly Lys Asp Val Arg Tyr Leu
 785 790 795 800

Gly Pro Gly Ser Asn Leu Thr Ser Ala Pro Val Pro Ser Thr Thr Thr
 115 120 125
 Arg Ser Leu Thr Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro
 130 135 140
 Met Leu Ile Glu Phe Asn Ile Pro Val Asp Leu Lys Leu Ile Glu Gln
 145 150 155 160
 Gln Asn Pro Lys Val Lys Leu Gly Gly Arg Tyr Thr Pro Met Asp Cys
 165 170 175
 Ile Ser Pro His Lys Val Ala Ile Ile Ile Leu Phe Arg Asn Arg Gln
 180 185 190
 Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Met Val Gln Arg
 195 200 205
 Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Glu Ser
 210 215 220
 Met Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Lys Glu Ala Leu
 225 230 235 240
 Lys Asp Tyr Asp Tyr Asn Cys Phe Val Phe Ser Asp Val Asp Leu Ile
 245 250 255
 Pro Met Asn Asp His Asn Thr Tyr Arg Cys Phe Ser Gln Pro Arg His
 260 265 270
 Ile Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln
 275 280 285
 Tyr Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Ser Ile
 290 295 300
 Asn Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp
 305 310 315 320
 Ile Tyr Asn Arg Leu Ala Phe Arg Gly Met Ser Val Ser Arg Pro Asn
 325 330 335
 Ala Val Ile Gly Lys Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys
 340 345 350
 Asn Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu
 355 360 365
 Thr Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Met Val Leu Glu
 370 375 380
 Val Gln Arg Tyr Pro Leu Tyr Thr Lys Ile Thr Val Asp Ile Gly Thr
 385 390 395 400

Pro Ser

<210> 28
 <211> 343
 <212> PRT
 <213> Sus scrofa

<220>

<223> full length porcine Gal beta-1,3-GalNAc
alpha-2,3-sialyltransferase 1 (ST3Gal1)

<400> 28

Met	Ala	Pro	Met	Arg	Lys	Lys	Ser	Thr	Leu	Lys	Leu	Leu	Thr	Leu	Leu		
1				5					10					15			
Val	Leu	Phe	Ile	Phe	Leu	Thr	Ser	Phe	Phe	Leu	Asn	Tyr	Ser	His	Thr		
			20					25					30				
Val	Val	Thr	Thr	Ala	Trp	Phe	Pro	Lys	Gln	Met	Val	Ile	Glu	Leu	Ser		
		35					40					45					
Glu	Asn	Phe	Lys	Lys	Leu	Met	Lys	Tyr	Pro	Tyr	Arg	Pro	Cys	Thr	Cys		
	50					55					60						
Thr	Arg	Cys	Ile	Glu	Glu	Gln	Arg	Val	Ser	Ala	Trp	Phe	Asp	Glu	Arg		
65					70					75					80		
Phe	Asn	Arg	Ser	Met	Gln	Pro	Leu	Leu	Thr	Ala	Lys	Asn	Ala	His	Leu		
				85					90					95			
Glu	Glu	Asp	Thr	Tyr	Lys	Trp	Trp	Leu	Arg	Leu	Gln	Arg	Glu	Lys	Gln		
			100					105					110				
Pro	Asn	Asn	Leu	Asn	Asp	Thr	Ile	Arg	Glu	Leu	Phe	Gln	Val	Val	Pro		
	115						120					125					
Gly	Asn	Val	Asp	Pro	Leu	Leu	Glu	Lys	Arg	Leu	Val	Ser	Cys	Arg	Arg		
	130					135					140						
Cys	Ala	Val	Val	Gly	Asn	Ser	Gly	Asn	Leu	Lys	Glu	Ser	Tyr	Tyr	Gly		
145					150					155					160		
Pro	Gln	Ile	Asp	Ser	His	Asp	Phe	Val	Leu	Arg	Met	Asn	Lys	Ala	Pro		
			165						170					175			
Thr	Glu	Gly	Phe	Glu	Ala	Asp	Val	Gly	Ser	Lys	Thr	Thr	His	His	Phe		
			180					185					190				
Val	Tyr	Pro	Glu	Ser	Phe	Arg	Glu	Leu	Ala	Gln	Glu	Val	Ser	Met	Ile		
		195					200					205					
Leu	Val	Pro	Phe	Lys	Thr	Thr	Asp	Leu	Glu	Trp	Val	Ile	Ser	Ala	Thr		
	210					215					220						
Thr	Thr	Gly	Thr	Ile	Ser	His	Thr	Tyr	Val	Pro	Val	Pro	Ala	Lys	Ile		
225					230					235					240		
Lys	Val	Lys	Lys	Glu	Lys	Ile	Leu	Ile	Tyr	His	Pro	Ala	Phe	Ile	Lys		
			245						250					255			
Tyr	Val	Phe	Asp	Arg	Trp	Leu	Gln	Gly	His	Gly	Arg	Tyr	Pro	Ser	Thr		
		260						265					270				
Gly	Ile	Leu	Ser	Val	Ile	Phe	Ser	Leu	His	Ile	Cys	Asp	Glu	Val	Asp		
	275						280					285					
Leu	Tyr	Gly	Phe	Gly	Ala	Asp	Ser	Lys	Gly	Asn	Trp	His	His	Tyr	Trp		
	290					295					300						

Glu Asn Asn Pro Ser Ala Gly Ala Phe Arg Lys Thr Gly Val His Asp
 305 310 315 320

Gly Asp Phe Glu Ser Asn Val Thr Thr Ile Leu Ala Ser Ile Asn Lys
 325 330 335

Ile Arg Ile Phe Lys Gly Arg
 340

<210> 29

<211> 600

<212> PRT

<213> Homo sapiens

<220>

<223> human alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I (ST6GalNAcTI)

<400> 29

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
 1 5 10 15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
 20 25 30

Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His Gln Arg Thr
 35 40 45

Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala Lys Pro Lys Ser
 50 55 60

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
 65 70 75 80

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
 85 90 95

Thr Gly Asp Arg Gly Lys Glu Ala Asn Gln Ala Pro Pro Glu Glu Gln
 100 105 110

Asp Lys Val Pro His Thr Ala Gln Arg Ala Ala Trp Lys Ser Pro Glu
 115 120 125

Lys Glu Lys Thr Met Val Asn Thr Leu Ser Pro Arg Gly Gln Asp Ala
 130 135 140

Gly Met Ala Ser Gly Arg Thr Glu Ala Gln Ser Trp Lys Ser Gln Asp
 145 150 155 160

Thr Lys Thr Thr Gln Gly Asn Gly Gly Gln Thr Arg Lys Leu Thr Ala
 165 170 175

Ser Arg Thr Val Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala
 180 185 190

Lys Thr Leu Ile Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly
 195 200 205

Ala Val Ser Thr Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile
 210 215 220

Pro Pro Lys Glu Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe
225 230 235 240

Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg Leu Lys Ala Ala Asn Phe
245 250 255

Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu Lys Tyr Ser Phe Glu Ile
260 265 270

Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser Val Lys Ile Lys Ala Ser
275 280 285

Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu Pro Asn Leu Thr Leu Phe
290 295 300

Leu Asp Ser Arg His Phe Asn Gln Ser Glu Trp Asp Arg Leu Glu His
305 310 315 320

Phe Ala Pro Pro Phe Gly Phe Met Glu Leu Asn Tyr Ser Leu Val Gln
325 330 335

Lys Val Val Thr Arg Phe Pro Pro Val Pro Gln Gln Gln Leu Leu Leu
340 345 350

Ala Ser Leu Pro Ala Gly Ser Leu Arg Cys Ile Thr Cys Ala Val Val
355 360 365

Gly Asn Gly Gly Ile Leu Asn Asn Ser His Met Gly Gln Glu Ile Asp
370 375 380

Ser His Asp Tyr Val Phe Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr
385 390 395 400

Glu Gln Asp Val Gly Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe
405 410 415

Ser Leu Thr Gln Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn
420 425 430

Val Pro Leu Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr
435 440 445

Arg Asp Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met
450 455 460

Ser Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg
465 470 475 480

Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe Leu
485 490 495

Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp Gly Ala
500 505 510

His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu Leu Leu Thr
515 520 525

Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly Phe Ile Thr Glu
530 535 540

Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp Thr Ser Trp Lys Arg
 545 550 555 560

Leu Ile Phe Tyr Ile Asn His Asp Phe Lys Leu Glu Arg Glu Val Trp
 565 570 575

Lys Arg Leu His Asp Glu Gly Ile Ile Arg Leu Tyr Gln Arg Pro Gly
 580 585 590

Pro Gly Thr Ala Lys Ala Lys Asn
 595 600

<210> 30
 <211> 566
 <212> PRT
 <213> Gallus gallus

<220>
 <223> chicken alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I (ST6GalNAcTI)

<400> 30
 Met Gly Phe Leu Ile Arg Arg Leu Pro Lys Asp Ser Arg Ile Phe Arg
 1 5 10 15

Trp Leu Leu Ile Leu Thr Val Phe Ser Phe Ile Ile Thr Ser Phe Ser
 20 25 30

Ala Leu Phe Gly Met Glu Lys Ser Ile Phe Arg Gln Leu Lys Ile Tyr
 35 40 45

Gln Ser Ile Ala His Met Leu Gln Val Asp Thr Gln Asp Gln Gln Gly
 50 55 60

Ser Asn Tyr Ser Ala Asn Gly Arg Ile Ser Lys Val Gly Leu Glu Arg
 65 70 75 80

Asp Ile Ala Trp Leu Glu Leu Asn Thr Ala Val Ser Thr Pro Ser Gly
 85 90 95

Glu Gly Lys Glu Glu Gln Lys Lys Thr Val Lys Pro Val Ala Lys Val
 100 105 110

Glu Glu Ala Lys Glu Lys Val Thr Val Lys Pro Phe Pro Glu Val Met
 115 120 125

Gly Ile Thr Asn Thr Thr Ala Ser Thr Ala Ser Val Val Glu Arg Thr
 130 135 140

Lys Glu Lys Thr Thr Ala Arg Pro Val Pro Gly Val Gly Glu Ala Asp
 145 150 155 160

Gly Lys Arg Thr Thr Ile Ala Leu Pro Ser Met Lys Glu Asp Lys Glu
 165 170 175

Lys Ala Thr Val Lys Pro Ser Phe Gly Met Lys Val Ala His Ala Asn
 180 185 190

Ser Thr Ser Lys Asp Lys Pro Lys Ala Glu Glu Pro Pro Ala Ser Val
 195 200 205

Lys Ala Ile Arg Pro Val Thr Gln Ala Ala Thr Val Thr Glu Lys Lys
 210 215 220
 Lys Leu Arg Ala Ala Asp Phe Lys Thr Glu Pro Gln Trp Asp Phe Asp
 225 230 235 240
 Asp Glu Tyr Ile Leu Asp Ser Ser Ser Pro Val Ser Thr Cys Ser Glu
 245 250 255
 Ser Val Arg Ala Lys Ala Ala Lys Ser Asp Trp Leu Arg Asp Leu Phe
 260 265 270
 Leu Pro Asn Ile Thr Leu Phe Ile Asp Lys Ser Tyr Phe Asn Val Ser
 275 280 285
 Glu Trp Asp Arg Leu Glu His Phe Ala Pro Pro Tyr Gly Phe Met Glu
 290 295 300
 Leu Asn Tyr Ser Leu Val Glu Glu Val Met Ser Arg Leu Pro Pro Asn
 305 310 315 320
 Pro His Gln Gln Leu Leu Leu Ala Asn Ser Ser Ser Asn Val Ser Thr
 325 330 335
 Cys Ile Ser Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn Asn Ser
 340 345 350
 Gly Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe Arg Val Ser
 355 360 365
 Gly Ala Val Ile Lys Gly Tyr Glu Lys Asp Val Gly Thr Lys Thr Ser
 370 375 380
 Phe Tyr Gly Phe Thr Ala Tyr Ser Leu Val Ser Ser Leu Gln Asn Leu
 385 390 395 400
 Gly His Lys Gly Phe Lys Lys Ile Pro Gln Gly Lys His Ile Arg Tyr
 405 410 415
 Ile His Phe Leu Glu Ala Val Arg Asp Tyr Glu Trp Leu Lys Ala Leu
 420 425 430
 Leu Leu Asp Lys Asp Ile Arg Lys Gly Phe Leu Asn Tyr Tyr Gly Arg
 435 440 445
 Arg Pro Arg Glu Arg Phe Asp Glu Asp Phe Thr Met Asn Lys Tyr Leu
 450 455 460
 Val Ala His Pro Asp Phe Leu Arg Tyr Leu Lys Asn Arg Phe Leu Lys
 465 470 475 480
 Ser Lys Asn Leu Gln Lys Pro Tyr Trp Arg Leu Tyr Arg Pro Thr Thr
 485 490 495
 Gly Ala Leu Leu Leu Thr Ala Leu His Leu Cys Asp Arg Val Ser
 500 505 510
 Ala Tyr Gly Tyr Ile Thr Glu Gly His Gln Lys Tyr Ser Asp His Tyr
 515 520 525

Tyr Asp Lys Glu Trp Lys Arg Leu Val Phe Tyr Val Asn His Asp Phe
 530 535 540

Asn Leu Glu Lys Gln Val Trp Lys Arg Leu His Asp Glu Asn Ile Met
 545 550 555 560

Lys Leu Tyr Gln Arg Ser
 565

<210> 31
 <211> 495
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mouse
 alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I (ST6GalNAcTI)
 beginning at residue 32 of the native mouse protein

<400> 31
 Asp Pro Arg Ala Lys Asp Ser Arg Cys Gln Phe Ile Trp Lys Asn Asp
 1 5 10 15
 Ala Ser Ala Gln Glu Asn Gln Gln Lys Ala Glu Pro Gln Val Pro Ile
 20 25 30
 Met Thr Leu Ser Pro Arg Val His Asn Lys Glu Ser Thr Ser Val Ser
 35 40 45
 Ser Lys Asp Leu Lys Lys Gln Glu Arg Glu Ala Val Gln Gly Glu Gln
 50 55 60
 Ala Glu Gly Lys Glu Lys Arg Lys Leu Glu Thr Ile Arg Pro Ala Pro
 65 70 75 80
 Glu Asn Pro Gln Ser Lys Ala Glu Pro Ala Ala Lys Thr Pro Val Ser
 85 90 95
 Glu His Leu Asp Lys Leu Pro Arg Thr Pro Gly Ala Leu Ser Thr Arg
 100 105 110
 Lys Thr Pro Met Ala Thr Gly Ala Val Pro Ala Lys Lys Lys Val Val
 115 120 125
 Gln Ala Thr Lys Ser Pro Ala Ser Ser Pro His Pro Thr Thr Arg Arg
 130 135 140
 Arg Gln Arg Leu Lys Ala Ser Glu Phe Lys Ser Glu Pro Arg Trp Asp
 145 150 155 160
 Phe Glu Glu Glu Tyr Ser Leu Asp Met Ser Ser Leu Gln Thr Asn Cys
 165 170 175
 Ser Ala Ser Val Lys Ile Lys Ala Ser Lys Ser Pro Trp Leu Gln Asn
 180 185 190
 Ile Phe Leu Pro Asn Ile Thr Leu Phe Leu Asp Ser Gly Arg Phe Thr
 195 200 205

Gln Ser Glu Trp Asn Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe
 210 215 220
 Met Glu Leu Asn Gln Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro
 225 230 235 240
 Pro Val Arg Gln Gln Gln Leu Leu Leu Ala Ser Leu Pro Thr Gly Tyr
 245 250 255
 Ser Lys Cys Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn
 260 265 270
 Asp Ser Arg Val Gly Arg Glu Ile Asp Ser His Asp Tyr Val Phe Arg
 275 280 285
 Leu Ser Gly Ala Val Ile Lys Gly Tyr Glu Gln Asp Val Gly Thr Arg
 290 295 300
 Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln Ser Ile Leu
 305 310 315 320
 Ile Leu Gly Arg Arg Gly Phe Gln His Val Pro Leu Gly Lys Asp Val
 325 330 335
 Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asn Tyr Glu Trp Leu Glu
 340 345 350
 Ala Met Phe Leu Asn Gln Thr Leu Ala Lys Thr His Leu Ser Trp Phe
 355 360 365
 Arg His Arg Pro Gln Glu Ala Phe Arg Asn Ala Leu Asp Leu Asp Arg
 370 375 380
 Tyr Leu Leu Leu His Pro Asp Phe Leu Arg Tyr Met Lys Asn Arg Phe
 385 390 395 400
 Leu Arg Ser Lys Thr Leu Asp Thr Ala His Trp Arg Ile Tyr Arg Pro
 405 410 415
 Thr Thr Gly Ala Leu Leu Leu Leu Thr Ala Leu His Leu Cys Asp Lys
 420 425 430
 Val Ser Ala Tyr Gly Phe Ile Thr Glu Gly His Gln Arg Phe Ser Asp
 435 440 445
 His Tyr Tyr Asp Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His
 450 455 460
 Asp Phe Arg Leu Glu Arg Met Val Trp Lys Arg Leu His Asp Glu Gly
 465 470 475 480
 Ile Ile Trp Leu Tyr Gln Arg Pro Gln Ser Asp Lys Ala Lys Asn
 485 490 495

<210> 32
 <211> 363
 <212> PRT
 <213> Homo sapiens

<220>

<223> full length human core 1
UDP-galactose:N-acetylgalactosamine-alpha-R
beta-1,3-galactosyltransferase (Core 1 GalT1)

<400> 32

Met	Ala	Ser	Lys	Ser	Trp	Leu	Asn	Phe	Leu	Thr	Phe	Leu	Cys	Gly	Ser	
1				5					10					15		
Ala	Ile	Gly	Phe	Leu	Leu	Cys	Ser	Gln	Leu	Phe	Ser	Ile	Leu	Leu	Gly	
			20					25					30			
Glu	Lys	Val	Asp	Thr	Gln	Pro	Asn	Val	Leu	His	Asn	Asp	Pro	His	Ala	
		35					40					45				
Arg	His	Ser	Asp	Asp	Asn	Gly	Gln	Asn	His	Leu	Glu	Gly	Gln	Met	Asn	
	50					55					60					
Phe	Asn	Ala	Asp	Ser	Ser	Gln	His	Lys	Asp	Glu	Asn	Thr	Asp	Ile	Ala	
65					70					75					80	
Glu	Asn	Leu	Tyr	Gln	Lys	Val	Arg	Ile	Leu	Cys	Trp	Val	Met	Thr	Gly	
				85					90						95	
Pro	Gln	Asn	Leu	Glu	Lys	Lys	Ala	Lys	His	Val	Lys	Ala	Thr	Trp	Ala	
		100						105					110			
Gln	Arg	Cys	Asn	Lys	Val	Leu	Phe	Met	Ser	Ser	Glu	Glu	Asn	Lys	Asp	
		115					120					125				
Phe	Pro	Ala	Val	Gly	Leu	Lys	Thr	Lys	Glu	Gly	Arg	Asp	Gln	Leu	Tyr	
	130					135					140					
Trp	Lys	Thr	Ile	Lys	Ala	Phe	Gln	Tyr	Val	His	Glu	His	Tyr	Leu	Glu	
145					150					155					160	
Asp	Ala	Asp	Trp	Phe	Leu	Lys	Ala	Asp	Asp	Asp	Thr	Tyr	Val	Ile	Leu	
				165					170					175		
Asp	Asn	Leu	Arg	Trp	Leu	Leu	Ser	Lys	Tyr	Asp	Pro	Glu	Glu	Pro	Ile	
		180						185					190			
Tyr	Phe	Gly	Arg	Arg	Phe	Lys	Pro	Tyr	Val	Lys	Gln	Gly	Tyr	Met	Ser	
	195						200					205				
Gly	Gly	Ala	Gly	Tyr	Val	Leu	Ser	Lys	Glu	Ala	Leu	Lys	Arg	Phe	Val	
	210					215					220					
Asp	Ala	Phe	Lys	Thr	Asp	Lys	Cys	Thr	His	Ser	Ser	Ser	Ile	Glu	Asp	
225					230					235					240	
Leu	Ala	Leu	Gly	Arg	Cys	Met	Glu	Ile	Met	Asn	Val	Glu	Ala	Gly	Asp	
				245				250						255		
Ser	Arg	Asp	Thr	Ile	Gly	Lys	Glu	Thr	Phe	His	Pro	Phe	Val	Pro	Glu	
		260						265					270			
His	His	Leu	Ile	Lys	Gly	Tyr	Leu	Pro	Arg	Thr	Phe	Trp	Tyr	Trp	Asn	
		275					280					285				

Tyr Asn Tyr Tyr Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu
 290 295 300

Ala Val Ser Phe His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu
 305 310 315 320

Tyr Leu Val Tyr His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln
 325 330 335

Pro Thr Leu Pro Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys
 340 345 350

Asn Glu Asp Thr Lys Val Lys Leu Gly Asn Pro
 355 360

<210> 33

<211> 341

<212> PRT

<213> Drosophila melanogaster

<220>

<223> Drosophila core 1

UDP-galactose:N-acetylgalactosamine-alpha-R
 beta-1,3-galactosyltransferase (Core 1 GalT1)

<400> 33

Glu Phe Met Pro Tyr Asp Gly His Arg His Gly Asp Val Asn Asp Ala
 1 5 10 15

His His Ser His Asp Met Met Glu Met Ser Gly Pro Glu Gln Asp Val
 20 25 30

Gly Gly His Glu His Val His Glu Asn Ser Thr Ile Ala Glu Arg Leu
 35 40 45

Tyr Ser Glu Val Arg Val Leu Cys Trp Ile Met Thr Asn Pro Ser Asn
 50 55 60

His Gln Lys Lys Ala Arg His Val Lys Arg Thr Trp Gly Lys Arg Cys
 65 70 75 80

Asn Lys Leu Ile Phe Met Ser Ser Ala Lys Asp Asp Glu Leu Asp Ala
 85 90 95

Val Ala Leu Pro Val Gly Glu Gly Arg Asn Asn Leu Trp Gly Lys Thr
 100 105 110

Lys Glu Ala Tyr Lys Tyr Ile Tyr Glu His His Ile Asn Asp Ala Asp
 115 120 125

Trp Phe Leu Lys Ala Asp Asp Asp Thr Tyr Thr Ile Val Glu Asn Met
 130 135 140

Arg Tyr Met Leu Tyr Pro Tyr Ser Pro Glu Thr Pro Val Tyr Phe Gly
 145 150 155 160

Cys Lys Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala
 165 170 175

Gly Tyr Val Leu Ser Arg Glu Ala Val Arg Arg Phe Val Val Glu Ala
 180 185 190
 Leu Pro Asn Pro Lys Leu Cys Lys Ser Asp Asn Ser Gly Ala Glu Asp
 195 200 205
 Val Glu Ile Gly Lys Cys Leu Gln Asn Val Asn Val Leu Ala Gly Asp
 210 215 220
 Ser Arg Asp Ser Asn Gly Arg Gly Arg Phe Phe Pro Phe Val Pro Glu
 225 230 235 240
 His His Leu Ile Pro Ser His Thr Asp Lys Lys Phe Trp Tyr Trp Gln
 245 250 255
 Tyr Ile Phe Tyr Lys Thr Asp Glu Gly Leu Asp Cys Cys Ser Asp Asn
 260 265 270
 Ala Ile Ser Phe His Tyr Val Ser Pro Asn Gln Met Tyr Val Leu Asp
 275 280 285
 Tyr Leu Ile Tyr His Leu Arg Pro Tyr Gly Ile Ile Asn Thr Pro Asp
 290 295 300
 Ala Leu Pro Asn Lys Leu Ala Val Gly Glu Leu Met Pro Glu Ile Lys
 305 310 315 320
 Glu Gln Ala Thr Glu Ser Thr Ser Asp Gly Val Ser Lys Arg Ser Ala
 325 330 335
 Glu Thr Lys Thr Gln
 340

<210> 34
 <211> 341
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <223> Drosophila core 1
 UDP-galactose:N-acetylgalactosamine-alpha-R
 beta-1,3-galactosyltransferase (Core 1 GalT1)

<400> 34
 Glu Phe Met Pro Tyr Asp Gly His Arg His Gly Asp Val Asn Asp Ala
 1 5 10 15
 His His Ser His Asp Met Met Glu Met Ser Gly Pro Glu Gln Asp Val
 20 25 30
 Gly Gly His Glu His Val His Glu Asn Ser Thr Ile Ala Glu Arg Leu
 35 40 45
 Tyr Ser Glu Val Arg Val Leu Cys Trp Ile Met Thr Asn Pro Ser Asn
 50 55 60
 His Gln Lys Lys Ala Arg His Val Lys Arg Thr Trp Gly Lys Arg Cys
 65 70 75 80

<400> 35
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Ile Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Leu
 65 70 75 80
 Thr Pro Ser Lys Ala Phe Gln Glu Lys Leu Phe Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Phe Asn Gly Lys Leu Ile Gly Tyr Pro Val Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Val Lys Glu Ala Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Thr Leu Arg Ala Asn Gly
 130 135 140
 Lys Ser Ala Ile Met Trp Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Val Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Phe Glu Asn Gly Val
 165 170 175
 Tyr Asp Ala Lys Asn Val Gly Val Asn Asn Ala Gly Ala Gln Ala Gly
 180 185 190
 Leu Gln Phe Ile Val Asp Leu Val Lys Asn Lys His Ile Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Lys Ser Lys
 225 230 235 240
 Ile Asn Tyr Gly Val Thr Leu Leu Pro Thr Phe His Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Thr Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Thr Glu Phe Leu Glu Asn Tyr Leu Ile Thr Asp
 275 280 285
 Gln Gly Leu Ala Glu Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Phe Gln Glu Gln Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320

Thr Met Asp Asn Ala Thr Asn Gly Glu Ile Met Pro Asn Ile Pro Gln
325 330 335

Met Ala Ala Phe Trp Tyr Ala Thr Arg Ser Ala Val Leu Asn Ala Ile
340 345 350

Thr Gly Arg Gln Thr Val Glu Ala Ala Leu Asn Asp Ala Ala Thr Arg
355 360 365

Ile Thr Lys
370

<210> 36

<211> 369

<212> PRT

<213> Escherichia coli

<220>

<223> maltose binding protein (MBP)

<400> 36

Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
100 105 110

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
130 135 140

Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
165 170 175

Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
180 185 190

Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
195 200 205

Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365

Ser

<210> 37

<211> 381

<212> PRT

<213> *Pyrococcus furiosus*

<220>

<223> maltose binding protein (MBP)

<400> 37

Met Lys Ile Glu Glu Gly Lys Val Val Ile Trp His Ala Met Gln Pro
 1 5 10 15
 Asn Glu Leu Glu Val Phe Gln Ser Leu Ala Glu Glu Tyr Met Ala Leu
 20 25 30
 Ser Pro Glu Val Glu Ile Val Phe Glu Gln Lys Pro Asn Leu Glu Asp
 35 40 45
 Ala Leu Lys Ala Ala Ile Pro Thr Gly Gln Gly Pro Asp Leu Phe Ile
 50 55 60
 Trp Ala His Asp Trp Ile Gly Lys Phe Ala Glu Ala Gly Leu Leu Glu
 65 70 75 80
 Pro Ile Asp Glu Tyr Val Thr Glu Asp Leu Leu Asn Glu Phe Ala Pro
 85 90 95

Met Ala Gln Asp Ala Met Gln Tyr Lys Gly His Tyr Tyr Ala Leu Pro
 100 105 110
 Phe Ala Ala Glu Thr Val Ala Ile Ile Tyr Asn Lys Glu Met Val Ser
 115 120 125
 Glu Pro Pro Lys Thr Phe Asp Glu Met Lys Ala Ile Met Glu Lys Tyr
 130 135 140
 Tyr Asp Pro Ala Asn Glu Lys Tyr Gly Ile Ala Trp Pro Ile Asn Ala
 145 150 155 160
 Tyr Phe Ile Ser Ala Ile Ala Gln Ala Phe Gly Gly Tyr Tyr Phe Asp
 165 170 175
 Asp Lys Thr Glu Gln Pro Gly Leu Asp Lys Pro Glu Thr Ile Glu Gly
 180 185 190
 Phe Lys Phe Phe Phe Thr Glu Ile Trp Pro Tyr Met Ala Pro Thr Gly
 195 200 205
 Asp Tyr Asn Thr Gln Gln Ser Ile Phe Leu Glu Gly Arg Ala Pro Met
 210 215 220
 Met Val Asn Gly Pro Trp Ser Ile Asn Asp Val Lys Lys Ala Gly Ile
 225 230 235 240
 Asn Phe Gly Val Val Pro Leu Pro Pro Ile Ile Lys Asp Gly Lys Glu
 245 250 255
 Tyr Trp Pro Arg Pro Tyr Gly Gly Val Lys Leu Ile Tyr Phe Ala Ala
 260 265 270
 Gly Ile Lys Asn Lys Asp Ala Ala Trp Lys Phe Ala Lys Trp Leu Thr
 275 280 285
 Thr Ser Glu Glu Ser Ile Lys Thr Leu Ala Leu Glu Leu Gly Tyr Ile
 290 295 300
 Pro Val Leu Thr Lys Val Leu Asp Asp Pro Glu Ile Lys Asn Asp Pro
 305 310 315 320
 Val Ile Tyr Gly Phe Gly Gln Ala Val Gln His Ala Tyr Leu Met Pro
 325 330 335
 Lys Ser Pro Lys Met Ser Ala Val Trp Gly Gly Val Asp Gly Ala Ile
 340 345 350
 Asn Glu Ile Leu Gln Asp Pro Gln Asn Ala Asp Ile Glu Gly Ile Leu
 355 360 365
 Lys Lys Tyr Gln Gln Glu Ile Leu Asn Asn Met Gln Gly
 370 375 380

<210> 38
 <211> 412
 <212> PRT
 <213> Thermococcus litoralis

<220>

<223> maltose binding protein (MBP)

<400> 38

Met Lys Ile Glu Glu Gly Lys Ile Val Phe Ala Val Gly Gly Ala Pro
1 5 10 15
Asn Glu Ile Glu Tyr Trp Lys Gly Val Ile Ala Glu Phe Glu Lys Lys
20 25 30
Tyr Pro Gly Val Thr Val Glu Leu Lys Arg Gln Ala Thr Asp Thr Glu
35 40 45
Gln Arg Arg Leu Asp Leu Val Asn Ala Leu Arg Gly Lys Ser Ser Asp
50 55 60
Pro Asp Val Phe Leu Met Asp Val Ala Trp Leu Gly Gln Phe Ile Ala
65 70 75 80
Ser Gly Trp Leu Glu Pro Leu Asp Asp Tyr Val Gln Lys Asp Asn Tyr
85 90 95
Asp Leu Ser Val Phe Phe Gln Ser Val Ile Asn Leu Ala Asp Lys Gln
100 105 110
Gly Gly Lys Leu Tyr Ala Leu Pro Val Tyr Ile Asp Ala Gly Leu Leu
115 120 125
Tyr Tyr Arg Lys Asp Leu Leu Glu Lys Tyr Gly Tyr Ser Lys Pro Pro
130 135 140
Glu Thr Trp Gln Glu Leu Val Glu Met Ala Gln Lys Ile Gln Ser Gly
145 150 155 160
Glu Arg Glu Thr Asn Pro Asn Phe Trp Gly Phe Val Trp Gln Gly Lys
165 170 175
Gln Tyr Glu Gly Leu Val Cys Asp Phe Val Glu Tyr Val Tyr Ser Asn
180 185 190
Gly Gly Ser Leu Gly Glu Phe Lys Asp Gly Lys Trp Val Pro Thr Leu
195 200 205
Asn Lys Pro Glu Asn Val Glu Ala Leu Gln Phe Met Val Asp Leu Ile
210 215 220
His Lys Tyr Lys Ile Ser Pro Pro Asn Thr Tyr Thr Glu Met Thr Glu
225 230 235 240
Glu Pro Val Arg Leu Met Phe Gln Gln Gly Asn Ala Ala Phe Glu Arg
245 250 255
Asn Trp Pro Tyr Ala Trp Gly Leu His Asn Ala Asp Asp Ser Pro Val
260 265 270
Lys Gly Lys Val Gly Val Ala Pro Leu Pro His Phe Pro Gly His Lys
275 280 285
Ser Ala Ala Thr Leu Gly Gly Trp His Ile Gly Ile Ser Lys Tyr Ser
290 295 300

Asp Asn Lys Ala Leu Ala Trp Glu Phe Val Lys Phe Val Glu Ser Tyr
 305 310 315 320
 Ser Val Gln Lys Gly Phe Ala Met Asn Leu Gly Trp Asn Pro Gly Arg
 325 330 335
 Val Asp Val Tyr Asp Asp Pro Ala Val Val Ser Lys Ser Pro His Leu
 340 345 350
 Lys Glu Leu Arg Ala Val Phe Glu Asn Ala Val Pro Arg Pro Ile Val
 355 360 365
 Pro Tyr Tyr Pro Gln Leu Ser Glu Ile Ile Gln Lys Tyr Val Asn Ser
 370 375 380
 Ala Leu Ala Gly Lys Ile Ser Pro Gln Glu Ala Leu Asp Lys Ala Gln
 385 390 395 400
 Lys Glu Ala Glu Glu Leu Val Lys Gln Tyr Ser Lys
 405 410

<210> 39
 <211> 378
 <212> PRT
 <213> *Thermatoga maritime*

<220>
 <223> maltose binding protein (MBP)

<400> 39
 Met Lys Ile Glu Gln Thr Lys Leu Thr Ile Trp Ser Ser Glu Lys Gln
 1 5 10 15
 Val Asp Ile Leu Gln Lys Leu Gly Glu Glu Phe Lys Ala Lys Tyr Gly
 20 25 30
 Ile Pro Val Glu Val Gln Tyr Val Asp Phe Gly Ser Ile Lys Ser Lys
 35 40 45
 Phe Leu Thr Ala Ala Pro Gln Gly Gln Gly Ala Asp Ile Ile Val Gly
 50 55 60
 Ala His Asp Trp Val Gly Glu Leu Ala Val Asn Gly Leu Ile Glu Pro
 65 70 75 80
 Ile Pro Asn Phe Ser Asp Leu Lys Asn Phe Tyr Asp Thr Ala Leu Lys
 85 90 95
 Ala Phe Ser Tyr Gly Gly Lys Leu Tyr Gly Val Pro Tyr Ala Met Glu
 100 105 110
 Ala Val Ala Leu Ile Tyr Asn Lys Asp Tyr Val Asp Ser Val Pro Lys
 115 120 125
 Thr Met Asp Glu Leu Ile Glu Lys Ala Lys Gln Ile Asp Glu Glu Tyr
 130 135 140
 Gly Gly Glu Val Arg Gly Phe Ile Tyr Asp Val Ala Asn Phe Tyr Phe
 145 150 155 160

Pro Gln Thr Ala Ala Thr Gly Asp Gly Pro Asp Ile Val Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Glu Ala Gly Leu Leu Val Glu Ile
 65 70 75 80
 Lys Pro Ser Ala Lys Ile Gln Glu Gly Ile Val Asp Phe Ala Trp Asp
 85 90 95
 Ala Val Lys Tyr Asn Gly Lys Ile Ile Gly Tyr Pro Ile Ala Val Glu
 100 105 110
 Ser Leu Ser Leu Ile Tyr Asn Lys Asp Leu Val Pro Asn Pro Pro Lys
 115 120 125
 Ser Trp Glu Glu Val Ala Glu Leu Asp Ala Lys Leu Lys Lys Glu Gly
 130 135 140
 Lys Ser Ala Ile Met Trp Asn Leu Lys Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Met Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Gly Val Asp Gly
 165 170 175
 Tyr Asp Val Lys Asp Ala Gly Ile Asn Asn Lys Gly Val Lys Asp Ala
 180 185 190
 Met Asn Phe Val Lys Gly Leu Val Asp Lys Gly Val Ile Ser Pro Asp
 195 200 205
 Met Asp Tyr Ser Val Ser Glu Ser Ala Phe Asn Gln Gly Asn Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ser Trp Gly Asn Ile Glu Lys Ser Gly
 225 230 235 240
 Ile Asn Tyr Gly Val Thr Thr Leu Pro Lys Phe Asn Gly Gln Ala Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Thr Ala Gly Ile Ser Thr Ala Ser Pro
 260 265 270
 Asn Lys Asp Leu Ala Val Glu Phe Ile Glu Asn Tyr Leu Leu Thr Asn
 275 280 285
 Asp Gly Leu Arg Met Val Asn Asn Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Asn Ser Phe Gln Arg Glu Leu Asp Ala Asp Ala Arg Ile Ala Ala
 305 310 315 320
 Thr Met Asp Asn Ala Met Asn Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Asn Ala Phe Trp Ser Ser Ala Lys Asn Ala Ile Ile Asn Ile Val
 340 345 350

Asp Gly Arg Gln Thr Val Asp Ala Ala Leu Ala Asp Ala Glu Lys Gln
 355 360 365

Met Thr Lys Pro
 370

<210> 41
 <211> 559
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human UDP-N-acetylgalactosaminyltransferase 1
 (GalNAcT1)

<400> 41
 Met Arg Lys Phe Ala Tyr Cys Lys Val Val Leu Ala Thr Ser Leu Ile
 1 5 10 15
 Trp Val Leu Leu Asp Met Phe Leu Leu Leu Tyr Phe Ser Glu Cys Asn
 20 25 30
 Lys Cys Asp Glu Lys Lys Glu Arg Gly Leu Pro Ala Gly Asp Val Leu
 35 40 45
 Glu Pro Val Gln Lys Pro His Glu Gly Pro Gly Glu Met Gly Lys Pro
 50 55 60
 Val Val Ile Pro Lys Glu Asp Gln Glu Lys Met Lys Glu Met Phe Lys
 65 70 75 80
 Ile Asn Gln Phe Asn Leu Met Ala Ser Glu Met Ile Ala Leu Asn Arg
 85 90 95
 Ser Leu Pro Asp Val Arg Leu Glu Gly Cys Lys Thr Lys Val Tyr Pro
 100 105 110
 Asp Asn Leu Pro Thr Thr Ser Val Val Ile Val Phe His Asn Glu Ala
 115 120 125
 Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Ile Asn Arg Ser Pro
 130 135 140
 Arg His Met Ile Glu Glu Ile Val Leu Val Asp Asp Ala Ser Glu Arg
 145 150 155 160
 Asp Phe Leu Lys Arg Pro Leu Glu Ser Tyr Val Lys Lys Leu Lys Val
 165 170 175
 Pro Val His Val Ile Arg Met Glu Gln Arg Ser Gly Leu Ile Arg Ala
 180 185 190
 Arg Leu Lys Gly Ala Ala Val Ser Lys Gly Gln Val Ile Thr Phe Leu
 195 200 205
 Asp Ala His Cys Glu Cys Thr Val Gly Trp Leu Glu Pro Leu Leu Ala
 210 215 220
 Arg Ile Lys His Asp Arg Arg Thr Val Val Cys Pro Ile Ile Asp Val
 225 230 235 240

Ile Ser Asp Asp Thr Phe Glu Tyr Met Ala Gly Ser Asp Met Thr Tyr
 245 250 255
 Gly Gly Phe Asn Trp Lys Leu Asn Phe Arg Trp Tyr Pro Val Pro Gln
 260 265 270
 Arg Glu Met Asp Arg Arg Lys Gly Asp Arg Thr Leu Pro Val Arg Thr
 275 280 285
 Pro Thr Met Ala Gly Gly Leu Phe Ser Ile Asp Arg Asp Tyr Phe Gln
 290 295 300
 Glu Ile Gly Thr Tyr Asp Ala Gly Met Asp Ile Trp Gly Gly Glu Asn
 305 310 315 320
 Leu Glu Ile Ser Phe Arg Ile Trp Gln Cys Gly Gly Thr Leu Glu Ile
 325 330 335
 Val Thr Cys Ser His Val Gly His Val Phe Arg Lys Ala Thr Pro Tyr
 340 345 350
 Thr Phe Pro Gly Gly Thr Gly Gln Ile Ile Asn Lys Asn Asn Arg Arg
 355 360 365
 Leu Ala Glu Val Trp Met Asp Glu Phe Lys Asn Phe Phe Tyr Ile Ile
 370 375 380
 Ser Pro Gly Val Thr Lys Val Asp Tyr Gly Asp Ile Ser Ser Arg Val
 385 390 395 400
 Gly Leu Arg His Lys Leu Gln Cys Lys Pro Phe Ser Trp Tyr Leu Glu
 405 410 415
 Asn Ile Tyr Pro Asp Ser Gln Ile Pro Arg His Tyr Phe Ser Leu Gly
 420 425 430
 Glu Ile Arg Asn Val Glu Thr Asn Gln Cys Leu Asp Asn Met Ala Arg
 435 440 445
 Lys Glu Asn Glu Lys Val Gly Ile Phe Asn Cys His Gly Met Gly Gly
 450 455 460
 Asn Gln Val Phe Ser Tyr Thr Ala Asn Lys Glu Ile Arg Thr Asp Asp
 465 470 475 480
 Leu Cys Leu Asp Val Ser Lys Leu Asn Gly Pro Val Thr Met Leu Lys
 485 490 495
 Cys His His Leu Lys Gly Asn Gln Leu Trp Glu Tyr Asp Pro Val Lys
 500 505 510
 Leu Thr Leu Gln His Val Asn Ser Asn Gln Cys Leu Asp Lys Ala Thr
 515 520 525
 Glu Glu Asp Ser Gln Val Pro Ser Ile Arg Asp Cys Asn Gly Ser Arg
 530 535 540
 Ser Gln Gln Trp Leu Leu Arg Asn Val Thr Leu Pro Glu Ile Phe
 545 550 555

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<211> 4
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<220>
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peptide

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<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

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Ile Trp Val Leu
1

<210> 44
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 44
Arg Ala Ile Pro Asp
1 5

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 45
Thr Ser Val Val Ile
1 5

<210> 46
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 46
Phe His Asn Glu Ala
1 5

<210> 47
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 47
Leu Leu Arg Thr Val
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 48
Glu Ile Ile Leu Val Asp Asp
1 5

<210> 49
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 49
Gly Leu Ile Arg Ala Arg Leu Lys Gly Ala
1 5 10

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 50
 Val Ile Thr Phe Leu Asp Ala His Cys Glu Cys
 1 5 10
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<210> 51
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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 peptide

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<210> 52
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 <212> PRT
 <213> Artificial Sequence

<220>
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 peptide

<400> 52
 Pro Ile Ile Asp Val Ile
 1 5

<210> 53
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<220>
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<210> 54
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<220>
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 peptide

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 Pro Ile Lys Thr Pro
 1 5

<210> 55
<211> 6
<212> PRT
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<220>
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peptide

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Ile Ala Gly Gly Leu Phe
1 5

<210> 56
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<212> PRT
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<220>
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peptide

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1 5 10 15

Gln Cys Gly Gly Ser Leu Glu Ile Ile
20 25

<210> 57
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 57
Val Gly His Val Phe Arg Lys
1 5

<210> 58
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 58
Pro Tyr Thr Phe Pro Gly Gly Ser Gly
1 5

<210> 59
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide

 <400> 59
 Ala Glu Val Trp Met Asp Glu Phe Lys Asn Phe Phe Tyr
 1 5 10

<210> 60
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 <212> PRT
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 <220>
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 peptide

 <400> 60
 Cys Lys Pro Phe
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<210> 61
 <211> 9
 <212> PRT
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 <220>
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 peptide

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 Trp Tyr Leu Glu Asn Ile Tyr Pro Asp
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<210> 62
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 <220>
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 peptide

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 Val Gly Ile Phe
 1

<210> 63
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<220>
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 peptide

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 Gly Gly Asn Gln
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 <210> 64
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 <212> PRT
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 <220>
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 peptide

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 <210> 65
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
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 peptide

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 Ser Gln Gln Trp
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 <210> 66
 <211> 8
 <212> PRT
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 <220>
 <223> Description of Artificial Sequence:anti-FLAG
 antibody epitope tag, "FLAG tag"

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 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

 <210> 67
 <211> 6
 <212> PRT
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 <220>
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 affinity tag, polyhistidine purification tag, poly
 His, metal chelate affinity ligand

<400> 67
 His His His His His His
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<210> 68
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
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 amplification sense primer Sial 5'Tm

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<210> 69
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
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 amplification antisense primer Sial 3' Whole

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<210> 70
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification sense primer ST3BAMH1

<400> 70
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<210> 71
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification antisense primer ST3XBA1

<400> 71
 gcgctctaga tcagatacca ctgcttaagt 30

<210> 72
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR 5' primer
 ST3 BamH1 delta73

 <400> 72
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 <210> 73
 <211> 38
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 ST3 BamH1 delta85

 <400> 73
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 <210> 74
 <211> 35
 <212> DNA
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 <220>
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 ST3 BamH1 delta86

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 <210> 75
 <211> 30
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 primer ST3-Xho1

 <400> 75
 ggtctcctcg agtcagatac cactgcttaa 30

 <210> 76
 <211> 37
 <212> DNA
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 <220>
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 oligonucleotide GnT1 R120A C121H+

 <400> 76
 ccgcagcact gttcgggccc acctggacaa gctgctg 37

<210> 77
<211> 37
<212> DNA
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<220>
<223> Description of Artificial Sequence:mutagenic
oligonucleotide GtT1 R120A C121H-

<400> 77
cagcagcttg tccaggtggg cccgaacagt gctgcg 37

<210> 78
<211> 33
<212> DNA
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<220>
<223> Description of Artificial Sequence:mutagenic
oligonucleotide GtT1C123A+

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agcactgttc ggcgcgccct ggacaagctg ctg 33

<210> 79
<211> 33
<212> DNA
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<220>
<223> Description of Artificial Sequence:mutagenic
oligonucleotide GtT1C123A-

<400> 79
cagcagcttg tccagggcgc gccgaacagt gct 33

<210> 80
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<220>
<223> Description of Artificial Sequence:MuC-2-like
GalNAc peptide acceptor

<400> 80
Met Val Thr Pro Thr Pro Thr Pro Thr Cys
1 5 10

Supplemental Application Data Sheet

Application Information

Application number:: 10/587,769
Filing Date::
Application Type:: Regular
Subject Matter:: Utility
Title:: Methods of Refolding Mammalian
Glycosyltransferases
Attorney Docket Number:: 019957-016830US
Request for Early Publication:: No
Request for Non-Publication:: No
Total Drawing Sheets:: 54
Small Entity?:: Yes
Petition included?:: No
Secrecy Order in Parent Appl.: No

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Country of Residence:: US
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Country of mailing address:: US
Postal or Zip Code of mailing address:: 19144

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Country of mailing address:: US
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Middle Name:: F.

Family Name:: Johnson
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Postal or Zip Code of mailing address:: 19040

Applicant Authority Type:: Inventor
Primary Citizenship Country:: US
Status:: Full Capacity
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Middle Name:: James
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State or Province of mailing address:: PA
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Correspondence Information

Correspondence Customer Number:: 20350

Representative Information

Representative Customer Number:: 20350

Domestic Priority Information

Application::	Continuity Type::	Parent Application::	Parent Filing Date::
This Application	National Stage of	PCT/US2005/ 003856	02/04/05
PCT/US2005/ 003856	An Appn claiming benefit under 35 USC 119(e) of	60/627,406	11/12/04
PCT/US2005/ 003856	An Appn claiming benefit under 35 USC 119(e) of	60/599,406	08/06/04
PCT/US2005/ 003856	An Appn claiming benefit under 35 USC 119(e) of	60/542,210	02/04/04

Foreign Priority Information

Country:: Application number:: Filing Date::

Assignee Information

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